Conclusions: TEM-68 is the second complex mutant β-lactamase (CMT-2) found in a clinical isolate that expresses both ESBL and IR activities. Its production by a *K. pneumoniae* strain may result in a high level resistance to all β-lactam antibiotics except carbapenems.

MoP284 A countrywide spread and a long time persistence of an ESBL-producing *Klebsiella pneumoniae* strain

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Objectives: To study structure of the population of ESBL-producing *K. pneurnoniae* present in the environment of a single hospital ward over a period of 2 years.
Methods: Twelve *K. pneumoniae* isolates identified in 1996 and 9 isolates collected in 1998 were studied. All the isolates were recovered from patients in the PICU of the University Hospital in Wrocław and found to be ESBL producers. The isolates were typed by RAPD and PFGE approaches; their β-lactamase content was studied by IEF and the ESBL *in vitro* overlay assay. ESBL-encoding genes were identified by PCR; selected PCR products were sequenced.
Results: A remarkable diversity of 3 distinct RAPD and PFGE types could be observed among the isolates from 1996. The predominant type (about 60% of isolates) was further split into two subtypes and expressed either the pI 8.2 ESBL of the SHV family or the pI 6.0 TEM-47 enzyme, previously identified in *K. pneumoniae* isolates from hospitals in Warsaw (in 1996) and Łódź (in 1995). The isolates from Wrocław were found very closely related to TEM-47-producing strains from the other cities. In 1998 all but one isolates represented one of the subtypes of the epidemic strain and expressed exclusively the pI 8.2 SHV ESBL.
Conclusions: A single ESBL-producing *K. pneumoniae* strain has spread in 3 distant paediatric centres in Poland. In one of these it persisted over the period of at least 2 years and dominated the population of multiresistant *K. pneumoniae*. These findings may suggest a high epidemic potential of the strain.

MoP285 Resistance of *Streptococcus pyogenes* strains to macrolides and other antibiotics in Poland

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Objectives: To evaluate antimicrobial susceptibility of *Streptococcus pyogenes* strains isolated in Poland in 1999 as compared with the data from 1997–1998.
Methods: One hundred and thirty-three isolates of Group A beta-haemolytic streptococci (GABHS) were collected from 11 health care centres in Poland. The strains were recovered from throat swabs, skin, soft tissue, sputum and blood. Beta-haemolytic colonies were identified as *S. pyogenes* using a latex agglutination test (Streptex; Murex). MICs of 8 antimicrobials were determined by the standard broth microdilution procedure and interpreted according to NCCLS. Antibiotic susceptibility profile of the following drugs was studied: penicillin G, erythromycin, clarithromycin, azithromycin, spiramycin, clindamycin, moxifloxacin and tetracycline. All erythromycin-resistant *S. pyogenes* were retested by disc-diffusion method in order to determine their phenotypes of resistance to macrolidas, lincosamides and streptogramin B (MLSB).
Results: Out of all drugs used in the study the highest resistance was observed for tetracycline (62 strains, 46.6%). Resistance to erythromycin was detected in 17 isolates (12.7%). A majority of them (13 isolates) demonstrated the inducible MLSB-resistance phenotype and the remaining isolates expressed the MLSB-resistance constitutively. All the *S. pyogenes* strains were susceptible to penicillin.
Conclusions: The prevalence of macrolide-resistant *S. pyogenes* has increased in Poland from 3.9% in 1997 and 7.9% in 1998 to 12.7% in 1999. Since growing trend has been observed it is advisable to carry on the monitoring, especially because of the extensive use of macrolides in clinical practice.

MoP286 *Clostridium difficile* as a cause of community-acquired diarrhoea

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Clostridium difficile, a Gram-positive, anaerobic, spore-forming bacterium, has been recognised as a major cause of nosocomial diarrhoea in persons receiving antibiotic therapy. Few data on the incidence of *C. difficile* in community-acquired diarrhoea are available. Toxigenic strains of *C. difficile* produce two toxins, an enterotoxin A and a cytotoxin B. In order to demonstrate whether the *C. difficile* infection may be a community-acquired disease, we studied 402 faecal specimens from patients presented to the hospital with diarrhoea for the presence of toxins A and B. All these patients did not report recent history of antibiotic therapy or hospitalisation. For the detection of *C. difficile* toxins A and B an ELISA was used. All the specimens that were positive with ELISA were reexamined with VIDAS *Clostridium difficile* toxin A immunoassay (ELFA). Also, all faecal specimens were examined for all the other enteropathogenic agents. Of the 402 samples tested, 8 were found positive for toxins A + B (ELISA) (2%), from which 6 were positive with VIDAS method (toxin A) (1.2%). In these 8 cases no other enteropathogenic agent was found and *C. difficile* may be considered as the sole reason for diarrhoea. In conclusion, *C. difficile* as a cause of community-acquired diarrhoea is of very low frequency. However, outbreaks of community-acquired *C. difficile* diarrhoea have been reported. Also, in other studies, clinical isolates of toxin A-negative, toxin B-positive *C. difficile* have been reported.

P:14/2 – Surveillance of infectious diseases and antibiotic resistance - II

MoP287 Infection as a cause of death among elderly patients in an internal medicine ward: An analysis of 3 years

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Objectives: Infection is common among elderly people and highly contributes to morbidity and mortality. Because few data are available we analyse all dead elderly patients (EP) in an Internal Medicine ward over a 3-years period.
Methods: We reviewed the medical records of all patients admitted between january-1996 and december-1998. Special attention was made to type, aetiology, acquisition and direct contribution of infection to death.
Results: Of the 3686 admitted patients between january-96 and december-98, 362 died (9.8%). 196/362 (54.1%) were EP with an active infection at the moment of death. Median age was 85 y (range 65–111), 100 were women (51%). EP developed 240 episodes of infection (1.22 episodes/patient). In 165 cases (84.1%) death was directly caused by infection: 103 (62.4%) by a community-acquired infection and 62 (54.8%) due to nosocomial infections. The most frequent aetiologies were respiratory tract infection 166 (69.1%), urinary tract infection 52 (21.6%) and sepsis with no clear aetiology 11 (4.5%). Gram-positive cocci were the causal agent in 16 episodes (6.6%): *E. faecalis* 6, *S. aureus* 5, *S. pneumoniae* 2 and others 3; gram-negative bacilli in 55 (22.9%): *E. coli* 28, *P. aeruginosa* 14, Proteus spp 6, *Klebsiella* spp 2 and others 5. Sepsis signs were observed in 65 EP (33.2%) when admitted and in 23 (11.7%) at the time of death.
Conclusions: 1. Infection is a frequent event previous to death. 2. Respiratory tract infection was the most common site of infection related to death and gram-negative bacilli the main causal agents found.

MoP288 Diering resistance patterns in *S. aureus* nasal colonization by community versus hospital based sampling

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Objective: To determine *S. aureus* colonization rates and resistance to nafcillin (MRSA) and other antimicrobial drugs and to identify epidemiologic risk factors.
Methods: *S. aureus* nasal carriage was investigated in 468 individuals from a representative community-based sample of the urban poor in San Francisco between August and December 1999 and compared to a concurrent

hospital-based sample of MRSA (N = 141). The Hospital based sample was dichotomized into MRSA isolates obtained from outpatients clinics (O/P) and from inpatients within <72 after admission and MRSA isolates collected > 72 after hospital admission (nosocomial).
Results: 118 (25.2%) of the urban poor were colonized with S. aureus. Among the community sample of *S. aureus*, resistance to nafcillin (MRSA) was (8.5%), erythromycin (36.4%), ciprofloxacin (3.4%), Trimethoprim-Sulfamethoxazole (TMS) (14.4%). Gentamycin, linezolid, and vancomycin resistance was (0%).

		% Resistance among MRSA isolates by sample					
	(n)	ERY	TCN	CIPRO	CLINDA	GENTA	TMS
Community	10	60	0	10	0	0	10
Hospital O/P & <72 hrs	65	67	5.5	36	34	13	11
Nosocomial	76	91	6	81	75	9	6

4/10 of the community MRSAs had prior contact with hospital and displayed a more drug resistant pattern. Prior hospitalization in Outpatient population affected mainly resistance to Clindamycin (10.7% versus 21.6% hosp.) and TMS (3.6% versus 10.8%)
Conclusions: MRSA prevalence is low in the urban poor community and appears multidrug sensitive. Multi-Drug resistant MRSA increases with contact with the health care system.

MoP289 Bacterial flora of *Hirudo mdedicinalis* and their antibiotic sensitives in middle black sea region

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Objectives: The rate of infection complication of leech therapy is almost 20% in its applications, because *Hirudo medicinalis* has endosymbiotic bacteria. The aim of this study is to determine the bacterial flora of *H. medicinalis* and their antibiotic sensitivities in Middle Black Sea region.
Methods: Sixteen adult leeches collected from three different areas of Middle Black Sea region. They were rubbed onto blood agar (BA) plates directly under ether anesthesia to get surface cultures. Than leeches were sacrificed to get mouth and gut content cultures. Culture swabs were applied to BA, eosin methylen blue agar (EMB), and ampicillin blood agar (ABA) plates. Gut contents were applied immediately to anaerobe blood culture medium also. Isolated bacteria were identified with API 32 E, and API 20 NE, fermentative and non-fermentative ones respectively. Standard disk diffusion test was performed to isolated bacteria.
Results: Bacteria isolated in 15 of 16 leeches' surfaces, in 7 of 16 mouths, in 15 of 16 guts. Most common types of cultured bacteria were *Aeromonas spp.* (n = 27), *Ochrobacter anthropi* (n = 23), and non-fermenting Gram negative rod (n = 11) in 73 isolates. Isolates were susceptible to ceftazidime (100%), cefotaxime (100%) ciprofloxacin (100%), gentamicin (100%), trimethoprim/sulfamethoxazole (100%), piperacillin/tazobactam (98.6%) imipenem (98.6%), amoxicillin/clavulanate (97.3%), cefixime (93.2%), chloramphenicol (91.9%), cefazolin, (75.7%), sulbactam/ampicillin (64.9%), and ampicillin (51.3%).
Conclusion: Since leeches were carders of Aeromonas and other bacteria, appropriate antibiotic prophylaxis should be administrated to the patient. Antibacterial agents could be determined in resistance pattern of bacterial flora of regional *H. medicinalis*.

MoP290 *Neisseria meningitidis* carriage – Longitudinal study in Polish military units

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Investigation of the *Neisseria meningitidis* carrier state may significantly contribute to understanding of the epidemiology and pathogenesis of meningococcal disease. Such study in semi-closed adult communities, like military units has never been performed in Poland before.

Three surveillance trials were run in two military units during 1998–2000. Pharyngeal swabs were taken from young men, mostly 19–23 years old on the entry to military and then up to 2, 3 and 6 months of service. Pharyngeal swabs were taken from 489 men during 4–6 swabbing occasions. All together 81, 225 and 153 meningococcal isolates, belonging to 54, 124 and 89 different *N. meningitidis* strains respectively, were obtained during three trials. In the longest one, *N. meningitidis* was isolated from 24% and 60% recruits, on the entry to military and after 6 months of service, respectively. Fluctuation of meningococcal carriage status was observed during trial. *Neisseria meningitidis* serogroup B was the predominant - 29.6% of isolated strains, however 61.8% remaining strains were non-groupable. Type and subtype characterisations showed presence of 66 different phenotypes, the predominant was NG:21:P1.7 (16%). Decreased susceptibility to penicillin (MIC = 0.125–0.25 mg/L) was observed among 9 (3.4%) strains, MIC50 and MIC90 were 0.015 mg/L and 0.06 mg/L, respectively. All strains were susceptible to ciprofloxacin (MIC range 0.001–0.06 mg/L). Asymptotically carried *N. meningitidis* strains were phenotypically quite different from invasive meningococcal strains isolated in Poland (dominate phenotype B:22:P1.14).

MoP291 Prevalence of hepatitis A and E virus in a Tunisian population

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Objectives: To evaluate the Hepatitis E virus (HEV) prevalence in Tunisia, to specify the risk factors, the transmission modalities and an eventual association with others Hepatitis virus (A, B, C).
Methods: 527 serums were tested with a commercially available kit HEV-EIA (Abbott). Hepatitis A, B, C virus markers were determined by ELISA methods (Cobas Core-Roche II) from: 205 asymptomatic volunteer blood donors (AVBD), 49 hemodialysis patients, 20 cirrhotic patients (CP) and 253 healthy poeple (HP): 148 health related staff (HRS), 105 young individuals (YI) with different age classes (0.5–15 years).
Results

Group	YI	AVBD	HRS	HP	CP
Prevalence of Anti HEV IgG (%)	0	4.9	6.8	14	20
Prevalence of Anti HAV IgG (%)	44	100	98	98	100

Conclusions: These results provide evidence for the high HEV prevalence in hemodialysis and cirrhotic patients. The HEV infection is not now a major public health problem in Tunisia. However HAV infection persist with more frequency than HEV one, particulary in young population.

MoP292 Epidemiology of bacteremia in adults during 1998–1999

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Objectives: To study the epidemiology of bacteremia during 1998–1999.
Methods: 735 blood cultures were examined by Bactec system (Becton Dickinson) from 517 patients aged 15–94 years. The median age of patients with bacteremia was 76 years. The identification of the isolated bacteria was performed by standard methods and the API systems (bioMerieux). The susceptibility testing was carried out by disk diffusion method.
Results: Positive cultures were found in 72 patients (13.9%) from which 79 microbial strains were isolated. *E. coli* was the most frequently isolated bacterium (50.6%) followed by *Enterococcus spp* (10.1%) and other in small numbers. Of *E. coli* isolates 32.5% were resistant to ampicillin, 25% to trimethoprime/sulfamethoxazole, 2.5% to cefuroxime, 0% to cefotaxime, 2.5% to ciprofloxacin and 0% to aminoglycosides. In 22 patients (36.6%) the bacteremia was hospital acquired. Average nursery time of patients with community acquired bacteremia was 12.4 days whereas those with hospital acquired bacteremia 21.6 days. The patients with bacteremia were suffering from urinary tract infections (27.8%), glomerulonefritis (2.8%), infections of biliary tract (20.8%) and pneumonia (5.5%). In 8.3% of the patients bacteremia was polymicrobial. Mortality rage was 9.7%.
Conclusions: The frequency of bacteremia was 13.9%. The most frequently isolated bacterium was *E. coli*. The most common underlying disease was urinary tract infections.

MoP293 Molecular epidemiology of streptomycin and sulfonamide resistance in *Salmonella* Typhimurium during 1989–1997 in Greece

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Objective: The aim of this study was to investigate genotypic relationships among isolates belonging to the most common antibiotic resistance phenotypes of *Salmonella* Typhimurium and susceptible isolates, from human, animal, food and environmental sources.
Material and methods: The resistance rates of 328 *S.* Typhimurium isolates to seventeen antibiotics were determined by the NCCLS disk diffusion method. The most frequent resistance phenotype was streptomycin/sulfonamides. Twenty four isolates belonged to this phenotype, whilst ten and five isolates were resistant only to streptomycin or sulfonamides, respectively; together, these constituted group I. Group II consisted of 36 susceptible isolates, for comparison. Chromosomal fingerprints of these isolates were generated by pulsed-field gel electrophoresis (PFGE) of *Xba*I-restricted genomic DNA.
Results: Nine PFGE types were observed in group I and ten in group II. Five types were common in both groups, with three of them being predominant: types A, B and C were represented by 10%, 28%, 28% of group I isolates and 14%, 42%, 8% of group II isolates, respectively. Six of the PFGE types that were specific to each group belonged to non-human isolates.
Conclusions: Antibiotic resistant and susceptible *S.* Typhimurium isolates displayed common as well as specific PFGE types. The majority of the rare and specific types were represented exclusively in isolates of non-human origin.

MoP294 Dominance of two M-types among erythromycin-resistant Group A haemolytic streptococci

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Objectives: To study the M-types of Group A haemolytic streptococci (GAS), that were susceptible or resistant to erythromycin (EryS and EryR).
Materials and Methods: A total of 70 GAS isolates, 49 EryR and 21 EryS, obtained during the period 10/97 to 10/98 at the two main children's hospitals of Athens, were included in the study. Antibiotic susceptibility to penicillin G, erythromycin and clindamycin was tested by a disk diffusion method according to NCCLS standards. Serotyping was performed with M-antisera and by *emm* gene capture ELISA.
Results: The majority of EryR isolates were from pharyngeal and nasal specimens (57% and 30%, respectively) while EryS isolates were mostly from pharyngeal specimens (70%). Serotyping showed a dominance of two M-types, M22 and M84, among EryR isolates (31% and 41%, respectively). The remaining EryR isolates belonged to M77, M4 and M12 (6, 4 and 2 isolates, respectively). Two isolates remained untypeable. EryS isolates belonged to M1, M5, M12, M77, M3, M4, M13 and M2 (5, 4, 3, 3, 2, 2, 1 and 1 isolates, respectively). No EryS isolates belonged to the M22 and M84 types.
Conclusions: Compared with EryS, more EryR isolates were isolated from nasal specimens. Two M-types, M22 and M84, were dominant among EryR isolates. In contrast, there was no single dominant M-type among the EryS isolates. It would therefore seem likely that erythromycin resistance among Greek GAS isolates is at least partly due to the spread of few specific M-types resistant to the antibiotic.

MoP295 Antibiotic resistance in coagulase negative staphylococci isolated from young adults in Hong Kong

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Objectives: To determine levels of antibiotic resistance in coagulase negative staphylococci (CNS) carded in healthy young adults in Hong Kong.
Methods: Predominant strains of CNS were isolated from the nares of 70 young adults in training for health care posts in Hong Kong. Questionnaires were administered to investigate recent antibiotic usage, age and sex. Antibiotypes (for 12 antimicrobial agents) were determined according to NCCLS criteria.
Results: The most common isolates were *Staphylococcus epidermidis* (75%), *S. hominis* (12.7%) and *S. caprae* (7%). 56% of strains were penicillin resistant, and 30%, 17%, 11% were resistant to tetracycline, erythromycin, and chloramphenicol, respectively. There were low levels of resistance to gentamicin, trimethoprim and methicillin. One strain showed intermediate resistance to glycopeptides. 41% of strains demonstrated several combinations of multiple. Analysis of questionnaires showed a significant association (OR = 5.85) between the carriage of multi-resistant strains and recent antibiotic usage.
Conclusions: High levels of antibiotic resistance were detected in the CNS of young adults training for health care posts in Hong Kong. The carriage of antibiotic resistant strains in normal flora of health care workers has important consequences both as a source of cross-infection in immunocompromised patients and as a source of resistance genes which may transfer to *S. aureus*. Recent antibiotic usage is a risk factor for carriage of multi-resistant CNS strains.

MoP296 Epidemiology of pertussis infection in St. Petersburg and Russia

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Objective: A comparative analysis of *Bordetella pertussis* strains isolated in St. Petersburg.
Methods: Epidemiological, bacteriological and immunological methods. Ribotyping (Regnault *et al.* 1995) and Arbitrary Primed PCR of the selection of 26 strains isolated in 1997–1999 in northwestern Russia.
Results: The rate of pertussis incidence in St. Petersburg constantly exceeds the average level for Russia (57.5 and 19.1/100 000 in 1998). 3–6 year old children form the basic group of infected due to the low level of immunization during few previous years. Serotype circulation in St. Petersburg is dynamic: frequency of isolation for serotype 1.2.3 is decreasing due to increasing percentage of immunized population. The same parameters for serotypes 1.2.0 and 1.0.3 are being equalized (45% and 49%). Both applied genotyping methods failed to reveal any interstrain difference.
Conclusions: The pertussis infection in St. Petersburg is mainly caused by *B. pertussis* serotypes 1.2.0 and 1.0.3 (94% together). Ribotyping and AP-PCR typing did not distinguish within *B. pertussis* that reflects the homogeneity of this species in the genome loci concerned.

MoP297 The recent emergence of ampicillin/quinolone resistant enterococci in Sweden appears to reflect a nation-wide clonal *E. faecium* outbreak

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Background: In a recent screening of 841 hospitalized (n = 27 centers) and 670 outpatients (n = 20 centers) the fecal carriage rate of ampicillin resistant enterococci (ARE) was 21.5% and 6%, respectively. All ARE were *E. faecium* and usually resistant also to quinolones and macrolides (Torell *et al.* J C M 1999;37:3509–13).
Objective: To clarify the clonality of ARE in Sweden.
Methods: All 220 fecal ARE and 175 matched ampicillin susceptible *E. faecium* (ASE) isolates were typed using the semiautomated and computerized PhenePlate (PhP) system. We also typed the only ARE isolate found in fecal specimens from 250 healthy individuals at 25 centers in 1990 and 25 clinical ARE isolates obtained from two hospitals 1993–1994. Isolates with a similarity of PhP fingerprints of > =0.95 were regarded to belong to the same cluster.
Results: The 220 fecal ARE isolates were heavily dominated by one PhP cluster (72% of hospital and 54% of community ARE isolates, mean

similarity of types 0.96–0.97) and comprised only 23 types and clusters. In contrast, the 175 matching ASE isolates were much more heterogenous, comprised 77 types/clusters (mean similarity 0.71) and included 3 isolates that belonged to the same PhP cluster as the dominating ARE cluster and thus may represent its ancestor. This cluster dominated even more among the 1993–1994 clinical ARE isolates (84%) and included also the single fecal ARE isolate from 1990. PFGE typing of a subset of isolates verified that the ARE isolates were much more closely related than the ASE isolates (mean similarity of types according to Gel Compar (0.6 *vs* 0.1).
Conclusion: See title.

MoP298 Characterisation of HCV genotype 4 heterogeneity and relationship with geographical distribution and category of patients

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Objectives: HCV genotype 4 is circulating in Europe at low rate. The characteristics of subtype variability for this genotype were investigated in different Italian regions.
Methods and: results: 28 HCV genotype 4 isolates were identified from 736 HCV-RNA positive sera in seroepidemiological studies performed in 4 different regions of North, South Italy and Sardinia. 24 (86%) were classified by phylogenetic analysis of E1 genome region (915–1128) as belonging to subtype 4d (Neighbour Joining Method). 3 isolates classified as subtype 4a were detected in haemophilic patients, possibly related to infections from blood products. One isolate classified as a new subtype derived from an Eritrean patient subjected to haemodialysis.

Very high genome homogeneity (mean variability 4.3%) was shown by genetic comparisons (DNA Dist Programs Phylip Package) for all the 4d isolates relative to the studies performed in Veneto, Calabria and Sardinia and originated from subjects of general population and outpatients (19 subtype 4d isolates out of 24). In contrast a considerable degree of heterogeneity, both intragroup and with the other groups (mean variability 8.2% and 8.7%, respectively) was observed among subtype 4d isolates identified in the patients of a haemodialysis center in Apulia region.
Conclusions: The subtype 4d resulted highly prevalent and endemic among HCV genotype 4 infections in Italy. The level of viral heterogeneity can be related to the modality of the infection and exposure to reinfections, as well as to the length of the period of past endemicity.

MoP299 Large variation in antibiotic usages between European countries

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Objectives: Comparative data on the consumption of antibiotics between countries are scarce. The objective of this study was to obtain figures on antibiotic sales to outpatients and hospitals from the countries in the European Union during 1993 and 1997.
Methods: The figures for Denmark were obtained from the Nordic Council of medicines, figures from Sweden from the National Corporation of Swedish Pharmacies. For the remaining countries figures were purchased from IMS Global services. This company collects data from different sources which are projected to a national level estimate and given as weight (kilograms). The figures for the Nordic countries were given as defined daily dosages (DDD) according to the ATC classification of the WHO. To make the data comparable with the figures from the Nordic countries, the IMS data were converted to DDD:s and related to the population size in the different countries (1000 inhabitants per day: TID).
Results: Comparative data from outpatient and hospital sale were available from 14 and 9 countries respectively. An increase in total antibiotic sales between 1993 and 1997 occurred in 9/14 and 7/9 countries respectively. There was a large variation in antibiotic usage between i countries. In 1997 the sales to outpatients varied between 8.9 to 36.5 DDD/TID. The 4 countries with the highest consumption were France, Spain Portugal and Belgium and the 4 with the lowest usage the Netherlands, Denmark, Sweden and Germany. The hospital usage varied between 1.2 and 3.2 DDD/TID. Details on differences in usage for different antibiotic classes will be presented.

MoP300 Lyme borreliosis in Western Russia

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Objectives: To analyze data on epidemiological characteristics of Lyme Borreliosis (LB) in the Western part of Russia and to identify genospecies of *Borrelia burgdorferi sensu lato*, circulating in several natural foci.
Methods: Epidemiological data on 305 cases of LB registered during 4 last years were analyzed. Sera from 232 patients and 667 province residents professionally exposed to infection were examined in indirect fluorescent antibody (IFA) test for detection of antibodies to *B. burgdorferi*. Ticks *I. ricinus* (*186 samples* were examined in polymerase chain reaction (PCR) to identify *Borrelia* genospecies.
Results: In Western part of Russia in Kaliningradskaya province 305 cases of LB were registered. The average morbidity rate of LB is 8.1 per 100 000 of inhabitants that 40 times higher than that relevant to tick-born encephalitis (TBE). Detection of antibodies to B. burgdorferi in 22% of people with professional exposure available was performed. The age of 72% of patients with LB was from 15 to 60 years. Percentage of children under 15 years old was 7%. Women developed disease 3.2 times more often than men. The number of ticks *J. ricinus* infected with *B. burgdorferi sensu lato* determined by PCR was 49. As to genospecies of *B. burgdorferi s. lato*, *B. afzelii* were identified in 37 ticks, *B. garinii* - in 4, *B. burgdorferi s. stricto* - *in 3, B. garinii* and *B. afzenii* simultaneously - in 4, *B. garinii* and *B. burgdorferi s. stricto* semultaneously - in 1 tick respectively.
Conclusion: Lyme Borreliosis is quite widely spread disease in the Western part of the Russia. Ticks *I. ricinus* turned to be infected with genospecies *B. afzelii* and *B. garinii* as well as with *B. burgdorferi sensu stricto*.

MoP301 A population-based study on influenza and clinical complications in the United Kingdom

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Objective: To analyze the relationship between chronic illnesses and the risk of getting influenza and influenza-related complications. Antibiotic usage attributable to influenza was also evaluated.
Methods: We conducted a large population-based study using the UK-based General Practice Research Database (GPRD) from 1991 to 1996. Using both a case-control and a cohort design, we analyzed risk factors, clinical complications and drug use for subjects with influenza diagnoses recorded in the database by age and presence of underlying chronic illnesses.
Results: We identified 141,293 subjects who had one or more diagnoses of influenza or influenza-like illness, and the same number of matched controls. The risk of getting influenza was particularly increased for subjects with chronic respiratory conditions (Odds ratio [OR] 1.6, 95% CI 1.5–1.7). Subjects with influenza were more likely to have a diagnosis of clinical complications than control subjects (OR 3.4, 95% CI 3.3–3.6). The risk of developing clinical complications was particularly increased for cases with chronic respiratory diseases (Relative Risk 1.9, 95% CI 1.80–2.0). Patients without underlying conditions accounted for 48% of all influenza-related complications. Overall, 45.2% of influenza cases and 5.3% of subjects in the matched control population received antibiotics in the 30-day time window immediately following the index date ($p < 0.0001$).
Conclusion: This study indicates that around half of the influenza-related complications occur in otherwise healthy individuals, however the risk of developing such complications was highest in the elderly/at risk population. Additionally, antibiotic usage was shown to be substantial in influenza patients.

MoP302 The spectrum of infectious diseases attended at the emergency ward of an urban general hospital

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Objectives: The infectious pathology and the antibiotic prescription to patients in the emergency ward were studied.
Methods: We revised the clinical records of all patients discharged during October 1999 from the general emergency ward of an urban teaching hospital, coveting a population of 500,000. Statistical analysis was performed with Stat View Statistical package.
Results: A total of 6,295 emergencies were attended during this month and a total of 5,470 (87%) were discharged. Infectious disease was diagnosed in 648/5,470 (11.84%). Mean age was 50.3 ± 23.0 years (18–97). 321 (49.54%) were males. The 5 most frequent presenting symptoms were: dyspnea 72 (11.11%), trunk and limb pain 62 (9.57%), abdominal pain 60 (9.26%), cough 52 (8.03%) and otalgia 50 (7.72%). Fever was present in 209 (32.2%). Complementary examinations were: chest x ray 231 (35.65%), blood analysis 205 (31.63%), urine analysis 91 (14.09%), blood arterial gas 57 (8.79%), and blood culture 29 (4.52%). Microbiological data was obtained in 12 (1.85%) cases. The most frequent diagnoses were: lower respiratory tract infection 127 (19.59%), skin and soft tissue infection 104 (16.04%), upper respiratory tract infection 99 (15.27%), acute gastroenteritis 84 (12.96%), and urinary infection in 57 (8.8%). 463 of the patients required antibiotic treatment: amoxicillyne-clavulanate 261 (54.21%), quinolones 86 (18.50%), macrolides 40 (8.6%), cloxacilline 36 (7.7%), cephalosporins 12 (2.5%).
Conclusions: Infectious diseases are very frequent pathology in the emergency ward. Dyspnea is the most frequent symptom, and bronchial and pulmonary pathology are the most prevalent entities observed. Microbiological diagnoses is rare. Amoxicillyne-clavulanate is the most frequently prescribed antibiotic.

MoP303 The etiologic spectrum of bacteriemia seen in a hematology unit

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Objectives: All episodes of bacteriemia and fungemia occurring among patients with high risk of severe sepsis observed in the Department of Hematology University Hospital in Cracow were analysed with regard to trends in causative organisms from 1993 to 1999. Three hundred and eleven patients with various degrees of immunosuppression, were retrospectively estimated in relation to the frequency of the blood-stream infections especially caused by new nosocomial pathogens.
Methods: A total number of 1328 blood cultures were tested using the automated-calorimetric BacT/Alert microbial detection system based on continuous-monitoring technology (Organon Teknika Corporation). The strains were identified in automatic ATB system using commercial strips with biochemical tests (bio-Merieux).
Results: Gram(+) and Gram(−) bacteria accounted for 53.9% and 34.4% of the episodes, respectively. There was a high incidence of invasive fungal infections-11.7%. The upward trend in Gram(+) bacteriemia appeared to be related to a significant increase in both *Enterococci* (0.0 to 6.4%) and *Viridans group Streptococci* (mainly *S. mitis*) (0.0 to 3.7%) respectively to the years. New groups of non-fermentative bacilli such as *Stenotrophomonas maltophilia* showed a tendency to increase and ranged from 3.7 to 11.9% during the past two years. Between 1993 and 1999 *Candida albicans* fungemias were not reported at all. A shift higher isolation of non-Candida spp. was observed. Two cases of fungemia caused by *Trichosporon beigelii* and *T. asahii* were described in 1998–1999. The proportion of poly versus monomicrobial infection has became changed from 25.0% vs 75.0% in 1996–1997 to more than 48.0% vs 51.2% in 1999.
Conclusions: Constant analysis of microbial evolution and localisation of infections should be essential element in control of hospital infections program.

MoP304 Prevalence of hepatitis C virus in pregnancy

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Objective: To assess the prevalence of anti-HCV and identify the risk factors for HCV infection in pregnant women.
Methods: 5.120 consecutive pregnant women attending the "Helena Venizelou" Maternity Hospital were screened for HCV antibodies by ELISA-2 (Abbott) and RIBA-2 (Innogenetics) methods. All women were interviewed to select relevant epidemiological data.
Results: The overall anti-HCV prevalence in pregnant women was 0.66% (34/5.120). The prevalence for Greek women was 0.61% (24/3.930) and for immigrants 0.84% (10/1.190). Risk factors for HCV infection were identified in 10 of the 34 anti-HCV positive women: a) 4 (11.8%) had been blood transfused, b) 4 (11.8%) were intravenous drug users, c) 2 (5.9%) were health care workers.
Conclusions: The prevalence of HCV infection is relatively low in Greek pregnant women but is higher in immigrants. The known risk factors were identified in only 29.4% for the anti-HCV(+) women.

MoP305 The results of a third-year period urine cultures in a Greek hospital

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Objective: The purpose of this study is to present our results from a third-year period urine cultures in our hospital.
Materials and Methods: During a 3-year period from 1997 to 1999 18.280 urine specimens were examined for bacterial pathogens in the microbiology laboratory at Hippokration General Hospital of Athens. Urine cultures and identification of bacterial pathogens were performed by standard microbiological methods. Antimicrobial susceptibility tests were performed by the agar diffusion method advocated by NCCLS.
Results: A 10% of the urine cultures were positive. There 1816 strains were isolated. The most frequently isolated pathogens were the Gram negative bacteria E. coli (60%), Klebsiella spp (19%), Proteus spp (7%), Pseudomonas spp (10%) and the gram positive cocci Enterococcus spp (11%) and Staphylococcus aureus (0.6%). As regards the sensitivity of the bacteria isolated, it is worth nothing that: four strains of enterococci spp were resistant to vancomycin and there is an increasing rate of resistance of enterococci against quinolones. There was a decreasing rate of resistance of gram negative bacteria against Ampicillin and Ampicillin-Clavulanic acid, while the resistance to cephalosporins remained at the same level.
Conclusion: It is of great importance to be a close cooperation between the committee of nosocomial infections and the clinicians in order to reduce the resistance to antibiotics.

P:14/3 – Surveillance of infectious diseases and antibiotic resistance - III

MoP306 Prevalence of macrolide - and aminoglycoside resistance genes in European *Staphylococcus aureus* isolates

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Objectives: To study the prevalence of macrolide and aminoglycoside resistance genes in *Staphylococcus aureus* isolates derived from 24 European university hospitals.
Methods: The prevalence of the macrolide resistance genes (*ermA, ermB, ermC, msrA/msrB, ereA, ereB*) and of the aminoglycoside resistance genes (*aac(6')-Ie + aph(2'')*, *ant(4')-Ia*, *aph(3')-IIIa*) was studied by PCR in 851 clinical erythromycin-resistant and 551 aminoglycoside-resistant *S. aureus* isolates, respectively.
Results: The *ermA* gene was more common in methicillin-resistant *S. aureus* (MRSA) (88%), mainly in strains with a constitutive MLSB expression, than in methicillin-susceptible *S. aureus* (MSSA) (38%), whereas *ermC* was predominant in MSSA (47%), mainly in strains with an inducible expression, and less so in MRSA (5%). The *ereB* gene was only found in MRSA (1%), while *ereA* was not detected. The *msrA/msrB* gene was only detectable